



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Murphy, Patricia
White, Marga
Olson, Sheri
Yoshikawa, Matthew
Jackson, Geoffrey
Eskanderi, Tara
Schryer, Brenda
Park, Michael

RECEIVED

OCT 25 2001

TECH CENTER 1600/2900

(ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES
OF THE HUMAN BRCA2 GENE

(iii) NUMBER OF SEQUENCES: 133

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Morgan, Lewis & Bockius LLP
(B) STREET: 1800 M St., NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/084,471
(B) FILING DATE: 22 May 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/055,784
(B) FILING DATE: 15 August 1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/064,926
(B) FILING DATE: 07 November 1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/065,367
(B) FILING DATE: 12 November 1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/071,715
(B) FILING DATE: 01 May 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reid G. Adler
(B) REGISTRATION NUMBER: 30,988
(C) REFERENCE/DOCKET NUMBER: 44921-5058-01-US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-467-7000
(B) TELEFAX: 202-467-7258

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 26...75
- (D) OTHER INFORMATION: Exon 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGGGATTTGC TTTGTTTTAT TTAGTCCTG TTGTTCTACA ATGTACACAT GTAACACCAC 60
AAAGAGATAA GTCAGGTATG ATTAAAAACA ATGCTTTTTT TTCTT 105

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...210
- (D) OTHER INFORMATION: Exon 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTGCTAA GTATTTATTC TTTGATAGAT TTAATTACAA GTCTTCAGAA TGCCAGAGAT 60
ATACAGGATA TGCGAATTAA GAAGAAACAA AGGCAACGCG TCTTTCCACA GCCAGGCAGT 120
CTGTATCTTG CAAAAACATC CACTCTGCCT CGAATCTCTC TGAAAGCAGC AGTAGGAGGC 180
CAAGTTCCTT CTGCGTGTTC TCATAAACAG GTATGTGT 218

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 34...221
- (D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

tttttctttt ttgtgtgtgt ttattttgtg tagctgtata cgtatggcgt ttctaaacat 60

tgcataaaaa ttaacagcaa aaatgcagag tcttttcagt ttcacactga agattatattt 120
 ggtaaggaaa gtttatggac tggaaaagga atacagttgg ctgatgggtg atggctcata 180
 ccctccaatg atggaaaggc tggaaaagaa gaattttata ggtactctat gcaaaaagat 240
 tgtgtgttaa cttttatg 258

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
 TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCCGC GCCGGGAGAA GCGTGAGGGG 120
 ACAGATTTGT GACCGGCGCG GTTTTGTGCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
 CTGGAGCGGA CTTATTACC AAGCATGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
 Met Pro Ile
 1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
 Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
 5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
 Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
 20 25 30 35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
 Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
 40 45 50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
 His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
 55 60 65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
 Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
 70 75 80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
 Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
 85 90 95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
 Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
 100 105 110 115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
 Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
 120 125 130

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389

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cont

His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val	
			375					380					385			
GTA	CCG	TCT	TTG	GCC	TGT	GAA	TGG	TCT	CAA	CTA	ACC	CTT	TCA	GGT	CTA	1437
Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu	Ser	Gly	Leu	
			390				395					400				
AAT	GGA	GCC	CAG	ATG	GAG	AAA	ATA	CCC	CTA	TTG	CAT	ATT	TCT	TCA	TGT	1485
Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile	Ser	Ser	Cys	
	405					410					415					
GAC	CAA	AAT	ATT	TCA	GAA	AAA	GAC	CTA	TTA	GAC	ACA	GAG	AAC	AAA	AGA	1533
Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu	Asn	Lys	Arg	
	420				425					430					435	
AAG	AAA	GAT	TTT	CTT	ACT	TCA	GAG	AAT	TCT	TTG	CCA	CGT	ATT	TCT	AGC	1581
Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg	Ile	Ser	Ser	
				440					445					450		
CTA	CCA	AAA	TCA	GAG	AAG	CCA	TTA	AAT	GAG	GAA	ACA	GTG	GTA	AAT	AAG	1629
Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val	Val	Asn	Lys	
			455				460						465			
AGA	GAT	GAA	GAG	CAG	CAT	CTT	GAA	TCT	CAT	ACA	GAC	TGC	ATT	CTT	GCA	1677
Arg	Asp	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys	Ile	Leu	Ala		
	470					475						480				
GTA	AAG	CAG	GCA	ATA	TCT	GGA	ACT	TCT	CCA	GTG	GCT	TCT	TCA	TTT	CAG	1725
Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser	Ser	Phe	Gln	
	485					490					495					
GGT	ATC	AAA	AAG	TCT	ATA	TTC	AGA	ATA	AGA	GAA	TCA	CCT	AAA	GAG	ACT	1773
Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro	Lys	Glu	Thr	
	500				505					510				515		
TTC	AAT	GCA	AGT	TTT	TCA	GGT	CAT	ATG	ACT	GAT	CCA	AAC	TTT	AAA	AAA	1821
Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn	Phe	Lys	Lys	
				520					525					530		
GAA	ACT	GAA	GCC	TCT	GAA	AGT	GGA	CTG	GAA	ATA	CAT	ACT	GTT	TGC	TCA	1869
Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr	Val	Cys	Ser	
			535				540						545			
CAG	AAG	GAG	GAC	TCC	TTA	TGT	CCA	AAT	TTA	ATT	GAT	AAT	GGA	AGC	TGG	1917
Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn	Gly	Ser	Trp	
		550					555					560				
CCA	GCC	ACC	ACC	ACA	CAG	AAT	TCT	GTA	GCT	TTG	AAG	AAT	GCA	GGT	TTA	1965
Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn	Ala	Gly	Leu	
	565					570					575					
ATA	TCC	ACT	TTG	AAA	AAG	AAA	ACA	AAT	AAG	TTT	ATT	TAT	GCT	ATA	CAT	2013
Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	Ala	Ile	His	
	580				585					590				595		
GAT	GAA	ACA	TCT	TAT	AAA	GGA	AAA	AAA	ATA	CCG	AAA	GAC	CAA	AAA	TCA	2061
Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	Gln	Lys	Ser	
				600					605					610		
GAA	CTA	ATT	AAC	TGT	TCA	GCC	CAG	TTT	GAA	GCA	AAT	GCT	TTT	GAA	GCA	2109
Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	Phe	Glu	Ala	

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615										620										625									
CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG	2157													
Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val														
		630					635					640																	
AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA	2205													
Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu														
		645					650					655																	
ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253													
Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr														
		660					665					670																	
TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301													
Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala														
					680										690														
AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349													
Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp														
					695									705															
TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397													
Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser														
							715							720															
AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445													
Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His														
		725												735															
CCA	GTA	CAA	CAT	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493													
Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser														
						745									755														
CAG	AAA	AGT	CTT	TTA	TAT	GAT	CAT	GAA	AAT	GCC	AGC	ACT	CTT	ATT	TTA	2541													
Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	Leu	Ile	Leu														
						760									770														
ACT	CCT	ACT	TCC	AAG	GAT	GTT	CTG	TCA	AAC	CTA	GTC	ATG	ATT	TCT	AGA	2589													
Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	Ile	Ser	Arg														
						775								785															
GGC	AAA	GAA	TCA	TAC	AAA	ATG	TCA	GAC	AAG	CTC	AAA	GGT	AAC	AAT	TAT	2637													
Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	Asn	Asn	Tyr														
						790								800															
GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685													
Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln														
						810								815															
GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733													
Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro														
						820						830			835														
CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781													
Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe														
						840									850														
AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829													
Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr														
						855									865														

ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC 2877
 Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe
 870 875 880

TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT 2925
 Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn
 885 890 895

AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT 2973
 Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr
 900 905 910 915

TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA 3021
 Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly
 920 925 930

GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG 3069
 Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu
 935 940 945

GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA 3117
 Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile
 950 955 960

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA 3165
 Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile
 965 970 975

GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA 3213
 Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly
 980 985 990 995

CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA 3261
 Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr
 1000 1005 1010

GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC 3309
 Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser
 1015 1020 1025

AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT 3357
 Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala
 1030 1035 1040

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055

AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075

GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105

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AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185

ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200

GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
 Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
 1205 1210 1215

TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
 Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
 1220 1225 1230 1235

AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
 Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
 1240 1245 1250

TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029
 Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
 1255 1260 1265

TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
 Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
 1270 1275 1280

AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125
 Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
 1285 1290 1295

ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
 Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
 1300 1305 1310 1315

AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
 Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
 1320 1325 1330

CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
 His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val
 1335 1340 1345

TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC 4317

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Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn
 1350 1355 1360
 ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG 4365
 Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln
 1365 1370 1375
 ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT 4413
 Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala
 1380 1385 1390 1395
 CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT 4461
 Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala
 1400 1405 1410
 ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
 Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
 1415 1420 1425
 TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
 Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
 1430 1435 1440
 AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
 Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
 1445 1450 1455
 TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
 Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
 1460 1465 1470 1475
 GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
 Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
 1480 1485 1490
 AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
 Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
 1495 1500 1505
 GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT 4797
 Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
 1510 1515 1520
 TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
 Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu
 1525 1530 1535
 GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
 Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
 1540 1545 1550 1555
 ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
 Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
 1560 1565 1570
 GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
 Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
 1575 1580 1585
 GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
 Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn

1590 1595 1600

CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
 Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
 1605 1610 1615

TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
 1620 1625 1630 1635

AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
 1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
 1655 1660 1665

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855

 AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875

 GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890

 GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949
 Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905

 CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920

 ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045
 Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu
 1925 1930 1935

 GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser
 1940 1945 1950 1955

 GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970

 GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985

 GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000

 GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015

 GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035

 CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050

 TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065

 ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477
 Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe
 2070 2075 2080

GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA 6525
 Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg
 2085 2090 2095
 CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG 6573
 Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu
 2100 2105 2110 2115
 CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA 6621
 His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys
 2120 2125 2130
 TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC 6669
 Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His
 2135 2140 2145
 TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA 6717
 Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln
 2150 2155 2160
 CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT 6765
 Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val
 2165 2170 2175
 TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT 6813
 Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly
 2180 2185 2190 2195
 AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT 6861
 Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val
 2200 2205 2210
 TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA 6909
 Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala
 2215 2220 2225
 GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT 6957
 Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser
 2230 2235 2240
 AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT 7005
 Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn
 2245 2250 2255
 GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG 7053
 Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu
 2260 2265 2270 2275
 CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT 7101
 Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn
 2280 2285 2290
 GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA 7149
 Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser
 2295 2300 2305
 AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT 7197
 Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His
 2310 2315 2320
 CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG 7245

His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys
 2325 2330 2335

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355

TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370

TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385

ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400

AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415

GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435

AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
 2440 2445 2450

AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
 Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
 2455 2460 2465

GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
 Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
 2470 2475 2480

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
 2485 2490 2495

AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
 2500 2505 2510 2515

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
 Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
 2520 2525 2530

CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
 Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
 2535 2540 2545

CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
 His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
 2550 2555 2560

ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
 Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile

D1
 cont

2565 2570 2575

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
 Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
 Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
 2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
 Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
 2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
 Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
 2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
 Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
 2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
 Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
 2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
 Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
 2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
 Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
 2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
 Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
 2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
 Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
 2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
 Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
 2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
 Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
 2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
 Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
 2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
 Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
 2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
 Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
 2885 2890 2895

GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
 Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
 2900 2905 2910 2915

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
 Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
 2920 2925 2930

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
 His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
 2935 2940 2945

ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
 Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
 2950 2955 2960

AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
 Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
 2965 2970 2975

AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
 Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
 2980 2985 2990 2995

TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
 Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
 3000 3005 3010

GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
 Ala Thr Ser Lys Ser Lys Ser Lys Glu Arg Ala Asn Ile Gln Leu
 3015 3020 3025

GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357
 Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
 3030 3035 3040

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
 Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
 3045 3050 3055

TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
 Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
 3060 3065 3070 3075
 GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
 Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
 3080 3085 3090
 TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549
 Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile
 3095 3100 3105
 GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597
 Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser
 3110 3115 3120
 AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645
 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe
 3125 3130 3135
 GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693
 Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe
 3140 3145 3150 3155
 CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741
 Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile
 3160 3165 3170
 CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789
 Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn
 3175 3180 3185
 GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837
 Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr
 3190 3195 3200
 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885
 Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser
 3205 3210 3215
 CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC 9933
 Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala
 3220 3225 3230 3235
 AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG 9981
 Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
 3240 3245 3250
 TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
 Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys
 3255 3260 3265
 AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077
 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val
 3270 3275 3280
 AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125
 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln
 3285 3290 3295
 CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173

Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys
 3300 3305 3310 3315
 GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330
 TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345
 AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360
 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375
 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395
 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410
 ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125

Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
 340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala

610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 1040
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100

D1
 cont

Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 1120
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 1200
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 1280
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 1360
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 1440
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 1520
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn

1585 1590 1595 1600
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 1680
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 1760
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 1840
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 1920
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 2000
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 2080

Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 2160
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 2240
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 2320
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 2400
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 2480
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 2560
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly

2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 2640
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
 2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 2720
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 2800
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 2880
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 2960
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 3040
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055

Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 3120
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 3200
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 3280
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 3360
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI2)

(ix) FEATURE:

(A) NAME/KEY: variation

(B) LOCATION: 3624

(D) OTHER INFORMATION: R = A or G. Xaa (amino acid position 1132) = Lys.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTGTG GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
Met Pro Ile
1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
20 25 30 35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
40 45 50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
55 60 65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
70 75 80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
85 90 95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
100 105 110 115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
120 125 130

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA 669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln
135 140 145

TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT 717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser
150 155 160

TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT 765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His
165 170 175

ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA 813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser

180 185 190 195

AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC 861
 Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val
 200 205 210

AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT 909
 Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala
 215 220 225

AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT 957
 Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn
 230 235 240

GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA 1005
 Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg
 245 250 255

GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA 1053
 Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys
 260 265 270 275

GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA 1101
 Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu
 280 285 290

GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT 1149
 Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser
 295 300 305

TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA 1197
 Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val
 310 315 320

AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT 1245
 Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp
 325 330 335

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA 1293
 Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val
 340 345 350 355

TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA 1341
 Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala
 360 365 370

CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT 1389
 His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val
 375 380 385

GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA 1437
 Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu
 390 395 400

AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT 1485
 Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys
 405 410 415

GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA 1533
 Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg
 420 425 430 435

AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC 1581
 Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser
 440 445 450

CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG 1629
 Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys
 455 460 465

AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA 1677
 Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala
 470 475 480

GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495

GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515

TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530

GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
 550 555 560

CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575

ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595

GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610

GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625

CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640

AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
 Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
 645 650 655

ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675

TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690

AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705

TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720

AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC 2445
 Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His
 725 730 735

CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC 2493
 Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser
 740 745 750 755

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA 2541
 Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu
 760 765 770

ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA 2589
 Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg
 775 780 785

GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT 2637
 Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr
 790 795 800

GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA 2685
 Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln
 805 810 815

GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA 2733
 Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro
 820 825 830 835

CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC 2781
 Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe
 840 845 850

AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT 2829
 Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr
 855 860 865

ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC 2877
 Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe
 870 875 880

TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT 2925
 Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn
 885 890 895

AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT 2973
 Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr
 900 905 910 915

TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA 3021

Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly
 920 925 930

GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG 3069
 Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu
 935 940 945

GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA 3117
 Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile
 950 955 960

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA 3165
 Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile
 965 970 975

GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA 3213
 Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly
 980 985 990 995

CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA 3261
 Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr
 1000 1005 1010

GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC 3309
 Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser
 1015 1020 1025

AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT 3357
 Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala
 1030 1035 1040

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055

AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075

GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105

AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAR CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro

DI cont

1160	1165	1170	
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu 1175 1180 1185			3789
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser 1190 1195 1200			3837
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe 1205 1210 1215			3885
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln 1220 1225 1230 1235			3933
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr 1240 1245 1250			3981
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265			4029
TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val 1270 1275 1280			4077
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285 1290 1295			4125
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300 1305 1310 1315			4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330			4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345			4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360			4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375			4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380 1385 1390 1395			4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400 1405 1410			4461

ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
 Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
 1415 1420 1425
 TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
 Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
 1430 1435 1440
 AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
 Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
 1445 1450 1455
 TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
 Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
 1460 1465 1470 1475
 GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
 Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
 1480 1485 1490
 AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
 Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
 1495 1500 1505
 GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT 4797
 Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
 1510 1515 1520
 TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
 Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu
 1525 1530 1535
 GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
 Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
 1540 1545 1550 1555
 ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
 Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
 1560 1565 1570
 GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
 Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
 1575 1580 1585
 GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
 Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn
 1590 1595 1600
 CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
 Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
 1605 1610 1615
 TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
 1620 1625 1630 1635
 AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
 1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
 1655 1660 1665
 GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680
 ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695
 GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715
 TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730
 CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745
 AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760
 TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775
 GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795
 GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810
 GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825
 AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840
 TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855
 AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875
 GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890
 GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949

Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905
 CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920
 ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045
 Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu
 1925 1930 1935
 GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser
 1940 1945 1950 1955
 GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970
 GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985
 GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000
 GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015
 GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035
 CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050
 TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065
 ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477
 Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe
 2070 2075 2080
 GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA 6525
 Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg
 2085 2090 2095
 CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG 6573
 Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu
 2100 2105 2110 2115
 CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA 6621
 His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys
 2120 2125 2130
 TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC 6669
 Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His

2135 2140 2145

TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA 6717
 Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln
 2150 2155 2160

CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT 6765
 Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val
 2165 2170 2175

TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT 6813
 Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly
 2180 2185 2190 2195

AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT 6861
 Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val
 2200 2205 2210

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA 6909
 Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala
 2215 2220 2225

GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT 6957
 Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser
 2230 2235 2240

AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT 7005
 Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn
 2245 2250 2255

GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG 7053
 Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu
 2260 2265 2270 2275

CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT 7101
 Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn
 2280 2285 2290

GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA 7149
 Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser
 2295 2300 2305

AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT 7197
 Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His
 2310 2315 2320

CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG 7245
 His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys
 2325 2330 2335

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355

TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370

TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385

D1
cont

ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400

AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415

GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435

AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
 2440 2445 2450

AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
 Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
 2455 2460 2465

GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
 Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
 2470 2475 2480

CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
 2485 2490 2495

AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
 2500 2505 2510 2515

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
 Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
 2520 2525 2530

CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
 Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
 2535 2540 2545

CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
 His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
 2550 2555 2560

ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
 Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile
 2565 2570 2575

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
 Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877

Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
 2870 2875 2880
 TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
 Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
 2885 2890 2895
 GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
 Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
 2900 2905 2910 2915
 TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
 Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
 2920 2925 2930
 CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
 His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
 2935 2940 2945
 ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
 Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
 2950 2955 2960
 AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
 Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
 2965 2970 2975
 AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
 Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
 2980 2985 2990 2995
 TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT 9261
 Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu
 3000 3005 3010
 GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA 9309
 Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu
 3015 3020 3025
 GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA 9357
 Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu
 3030 3035 3040
 ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA 9405
 Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys
 3045 3050 3055
 TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA 9453
 Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile
 3060 3065 3070 3075
 GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
 Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
 3080 3085 3090
 TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549
 Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile
 3095 3100 3105
 GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597
 Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser

3110 3115 3120

AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645
 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe
 3125 3130 3135

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693
 Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe
 3140 3145 3150 3155

CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741
 Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile
 3160 3165 3170

CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789
 Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn
 3175 3180 3185

GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837
 Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr
 3190 3195 3200

ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885
 Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser
 3205 3210 3215

CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC 9933
 Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala
 3220 3225 3230 3235

AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG 9981
 Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
 3240 3245 3250

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
 Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys
 3255 3260 3265

AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077
 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val
 3270 3275 3280

AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125
 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln
 3285 3290 3295

CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173
 Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys
 3300 3305 3310 3315

GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330

TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: variation
 (B) LOCATION: 1132
 (D) OTHER INFORMATION: Xaa = Lys (from codon AAR,
 R = A or G).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val

Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 1040
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 1120
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly

1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 1200
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 1280
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 1360
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 1440
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 1520
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 1600
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660

Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 1680
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 1760
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 1840
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 1920
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 2000
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 2080
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln

2145 2150 2155 2160
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 2240
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 2320
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 2400
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 2480
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 2560
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 2640

Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
 2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 2720
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 2800
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 2880
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 2960
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 3040
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 3120
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu

3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 3200
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 3280
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 3360
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
 TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
 ACAGATTGTG GACCGGCGCG GTTTTGTGCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
 CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
 Met Pro Ile

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	

GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA 1005
 Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg
 245 250 255

GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA 1053
 Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys
 260 265 270 275

GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA 1101
 Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu
 280 285 290

GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT 1149
 Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser
 295 300 305

TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA 1197
 Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val
 310 315 320

AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT 1245
 Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp
 325 330 335

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA 1293
 Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val
 340 345 350 355

TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA 1341
 Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala
 360 365 370

AAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT 1389
 Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val
 375 380 385

GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA 1437
 Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu
 390 395 400

AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT 1485
 Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys
 405 410 415

GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA 1533
 Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg
 420 425 430 435

AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC 1581
 Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser
 440 445 450

CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG 1629
 Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys
 455 460 465

AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA 1677
 Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala
 470 475 480

GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495

GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515

TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530

GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
 550 555 560

CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575

ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595

GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610

GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625

CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG 2157
 Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val
 630 635 640

AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA 2205
 Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu
 645 650 655

ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA 2253
 Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr
 660 665 670 675

TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA 2301
 Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala
 680 685 690

AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT 2349
 Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp
 695 700 705

TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC 2397
 Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser
 710 715 720

AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC 2445

Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His
 725 730 735
 CCA GTA CAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC 2493
 Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser
 740 745 750 755
 CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA 2541
 Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu
 760 765 770
 ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA 2589
 Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg
 775 780 785
 GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT 2637
 Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr
 790 795 800
 GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA 2685
 Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln
 805 810 815
 GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA 2733
 Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro
 820 825 830 835
 CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC 2781
 Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe
 840 845 850
 AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT 2829
 Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr
 855 860 865
 ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC 2877
 Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe
 870 875 880
 TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT 2925
 Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn
 885 890 895
 AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT 2973
 Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr
 900 905 910 915
 TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA 3021
 Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly
 920 925 930
 GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG 3069
 Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu
 935 940 945
 GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA 3117
 Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile
 950 955 960
 AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA 3165
 Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile

965 970 975

GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA 3213
 Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly
 980 985 990 995

CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA 3261
 Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr
 1000 1005 1010

GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC 3309
 Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser
 1015 1020 1025

AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT 3357
 Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala
 1030 1035 1040

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055

AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075

GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090

TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105

AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185

ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200

GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
 Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
 1205 1210 1215

TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
 Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
 1220 1225 1230 1235
 AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
 Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
 1240 1245 1250
 TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029
 Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
 1255 1260 1265
 TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
 Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
 1270 1275 1280
 AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125
 Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
 1285 1290 1295
 ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
 Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
 1300 1305 1310 1315
 AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
 Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
 1320 1325 1330
 CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
 His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val
 1335 1340 1345
 TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC 4317
 Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn
 1350 1355 1360
 ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG 4365
 Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln
 1365 1370 1375
 ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT 4413
 Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala
 1380 1385 1390 1395
 CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT 4461
 Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala
 1400 1405 1410
 ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
 Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
 1415 1420 1425
 TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
 Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
 1430 1435 1440
 AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
 Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
 1445 1450 1455

TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
1460 1465 1470 1475

GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
1480 1485 1490

AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
1495 1500 1505

GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT 4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
1510 1515 1520

TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu
1525 1530 1535

GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
1540 1545 1550 1555

ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
1560 1565 1570

GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
1575 1580 1585

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn
1590 1595 1600

CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
1605 1610 1615

TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
1620 1625 1630 1635

AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
1655 1660 1665

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
1670 1675 1680

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
1685 1690 1695

GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373

Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855

AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875

GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890

GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949
 Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905

CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920

ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045
 Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu
 1925 1930 1935

GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser

1940 1945 1950 1955

GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970

GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985

GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015

GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035

CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050

TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065

ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477
 Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe
 2070 2075 2080

GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA 6525
 Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg
 2085 2090 2095

CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG 6573
 Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu
 2100 2105 2110 2115

CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA 6621
 His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys
 2120 2125 2130

TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC 6669
 Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His
 2135 2140 2145

TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA 6717
 Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln
 2150 2155 2160

CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT 6765
 Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val
 2165 2170 2175

TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT 6813
 Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly
 2180 2185 2190 2195

AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT 6861
 Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val
 2200 2205 2210

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA 6909
 Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala
 2215 2220 2225

GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT 6957
 Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser
 2230 2235 2240

AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT 7005
 Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn
 2245 2250 2255

GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG 7053
 Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu
 2260 2265 2270 2275

CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT 7101
 Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn
 2280 2285 2290

GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA 7149
 Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser
 2295 2300 2305

AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT 7197
 Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His
 2310 2315 2320

CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG 7245
 His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys
 2325 2330 2335

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355

TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370

TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385

ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400

AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415

GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435

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 cont

AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
2440 2445 2450
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
2455 2460 2465
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
2470 2475 2480
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
2485 2490 2495
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
2500 2505 2510 2515
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
2520 2525 2530
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
2535 2540 2545
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
2550 2555 2560
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile
2565 2570 2575
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
2580 2585 2590 2595
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
2600 2605 2610
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
2615 2620 2625
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
2630 2635 2640
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
2645 2650 2655
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
2660 2665 2670 2675
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301

Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
2885 2890 2895

GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
2900 2905 2910 2915

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn

2920	2925	2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu 2935 2940 2945			9069
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950 2955 2960			9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965 2970 2975			9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980 2985 2990 2995			9213
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000 3005 3010			9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015 3020 3025			9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 3040			9357
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055			9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075			9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090			9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105			9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120			9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135			9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155			9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170			9741

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cont*

CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789
 Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn
 3175 3180 3185
 GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837
 Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr
 3190 3195 3200
 ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885
 Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser
 3205 3210 3215
 CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC 9933
 Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala
 3220 3225 3230 3235
 AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG 9981
 Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
 3240 3245 3250
 TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
 Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys
 3255 3260 3265
 AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077
 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val
 3270 3275 3280
 AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125
 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln
 3285 3290 3295
 CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173
 Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys
 3300 3305 3310 3315
 GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330
 TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345
 AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360
 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375
 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395
 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA
 Ile Thr Thr Lys Lys Tyr Ile
 3415

10485

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr

340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830

Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 1040
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 1120
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 1200
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 1280
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser

1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 1360
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 1440
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 1520
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 1600
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 1680
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 1760
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805

Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 1840
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 1920
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 2000
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 2080
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 2160
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 2240
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu

2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 2320
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 2400
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 2480
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 2560
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 2640
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
 2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 2720
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780

Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 2800
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 2880
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 2960
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 3040
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 3120
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 3200
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro

3265	3270	3275	3280
Pro Pro Val Ser	Pro Ile Cys Thr Phe	Val Ser Pro Ala Ala	Gln Lys
	3285	3290	3295
Ala Phe Gln Pro	Pro Arg Ser Cys Gly	Thr Lys Tyr Glu	Thr Pro Ile
	3300	3305	3310
Lys Lys Lys Glu	Leu Asn Ser Pro	Gln Met Thr Pro	Phe Lys Lys Phe
	3315	3320	3325
Asn Glu Ile Ser	Leu Leu Glu Ser	Asn Ser Ile Ala	Asp Glu Glu Leu
	3330	3335	3340
Ala Leu Ile Asn	Thr Gln Ala Leu	Leu Ser Gly Ser	Thr Gly Glu Lys
3345	3350	3355	3360
Gln Phe Ile Ser	Val Ser Glu Ser	Thr Arg Thr Ala	Pro Thr Ser Ser
	3365	3370	3375
Glu Asp Tyr Leu	Arg Leu Lys Arg	Arg Cys Thr Thr	Ser Leu Ile Lys
	3380	3385	3390
Glu Gln Glu Ser	Ser Gln Ala Ser	Thr Glu Glu Cys	Glu Lys Asn Lys
	3395	3400	3405
Gln Asp Thr Ile	Thr Thr Lys Lys	Tyr Ile	
3410	3415		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTGTG GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197

D
Cont

Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val
 310 315 320
 AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT 1245
 Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp
 325 330 335
 GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA 1293
 Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val
 340 345 350 355
 TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA 1341
 Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala
 360 365 370
 CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT 1389
 His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val
 375 380 385
 GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA 1437
 Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu
 390 395 400
 AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT 1485
 Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys
 405 410 415
 GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA 1533
 Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg
 420 425 430 435
 AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC 1581
 Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser
 440 445 450
 CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG 1629
 Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys
 455 460 465
 AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA 1677
 Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala
 470 475 480
 GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495
 GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515
 TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530
 GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545
 CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp

550 555 560

CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	

DI cont

GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln 805 810 815	2685
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro 820 825 830 835	2733
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe 840 845 850	2781
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr 855 860 865	2829
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe 870 875 880	2877
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895	2925
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915	2973
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930	3021
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945	3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960	3117
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975	3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995	3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010	3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025	3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040	3357

TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG 3405
 Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu
 1045 1050 1055
 AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT 3453
 Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser
 1060 1065 1070 1075
 GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA 3501
 Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu
 1080 1085 1090
 TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA 3549
 Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln
 1095 1100 1105
 AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT 3597
 Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser
 1110 1115 1120
 CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135
 AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155
 TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170
 TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185
 ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200
 GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
 Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
 1205 1210 1215
 TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
 Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
 1220 1225 1230 1235
 AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
 Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
 1240 1245 1250
 TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029
 Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
 1255 1260 1265
 TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
 Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
 1270 1275 1280
 AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125

Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
 1285 1290 1295
 ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
 Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
 1300 1305 1310 1315
 AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
 Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
 1320 1325 1330
 CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
 His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val
 1335 1340 1345
 TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC 4317
 Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn
 1350 1355 1360
 ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG 4365
 Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln
 1365 1370 1375
 ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT 4413
 Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala
 1380 1385 1390 1395
 CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT 4461
 Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala
 1400 1405 1410
 ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
 Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
 1415 1420 1425
 TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
 Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
 1430 1435 1440
 AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
 Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
 1445 1450 1455
 TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
 Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
 1460 1465 1470 1475
 GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
 Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
 1480 1485 1490
 AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
 Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
 1495 1500 1505
 GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT 4797
 Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
 1510 1515 1520
 TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
 Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu

1525 1530 1535

GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
 Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
 1540 1545 1550 1555

ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
 Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
 1560 1565 1570

GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
 Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
 1575 1580 1585

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
 Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn
 1590 1595 1600

CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
 Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
 1605 1610 1615

TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
 1620 1625 1630 1635

AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
 1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
 1655 1660 1665

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805
 Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855

AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875

GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890

GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949
 Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905

CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920

ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045
 Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu
 1925 1930 1935

GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser
 1940 1945 1950 1955

GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970

GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985

GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015

GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035

CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050

TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065

ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477
 Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe
 2070 2075 2080

GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA 6525
 Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg
 2085 2090 2095

CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG 6573
 Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu
 2100 2105 2110 2115

CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA 6621
 His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys
 2120 2125 2130

TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC 6669
 Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His
 2135 2140 2145

TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA 6717
 Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln
 2150 2155 2160

CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT 6765
 Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val
 2165 2170 2175

TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT 6813
 Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly
 2180 2185 2190 2195

AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT 6861
 Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val
 2200 2205 2210

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA 6909
 Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala
 2215 2220 2225

GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT 6957
 Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser
 2230 2235 2240

AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT 7005
 Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn
 2245 2250 2255

GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG 7053

Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu
 2260 2265 2270 2275
 CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT 7101
 Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn
 2280 2285 2290
 GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA 7149
 Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser
 2295 2300 2305
 AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT 7197
 Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His
 2310 2315 2320
 CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG 7245
 His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys
 2325 2330 2335
 GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355
 TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370
 TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385
 ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400
 AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415
 GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435
 AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
 2440 2445 2450
 AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
 Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
 2455 2460 2465
 GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
 Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
 2470 2475 2480
 CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
 2485 2490 2495
 AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr

2500	2505	2510	2515	
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT				7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val				
2520	2525	2530		
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA				7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys				
2535	2540	2545		
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC				7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His				
2550	2555	2560		
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA				7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile				
2565	2570	2575		
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT				8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala				
2580	2585	2590	2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT				8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp				
2600	2605	2610		
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC				8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile				
2615	2620	2625		
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT				8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala				
2630	2635	2640		
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA				8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg				
2645	2650	2655		
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA				8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile				
2660	2665	2670	2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT				8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser				
2680	2685	2690		
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA				8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys				
2695	2700	2705		
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT				8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp				
2710	2715	2720		
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC				8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val				
2725	2730	2735		
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA				8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly				
2740	2745	2750	2755	

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
 Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
 2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733
 Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser
 2820 2825 2830 2835

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA 8781
 Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala
 2840 2845 2850

GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT 8829
 Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr
 2855 2860 2865

AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA 8877
 Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro
 2870 2875 2880

TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA 8925
 Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln
 2885 2890 2895

GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT 8973
 Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala
 2900 2905 2910 2915

TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT 9021
 Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn
 2920 2925 2930

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA 9069
 His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu
 2935 2940 2945

ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA 9117
 Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser
 2950 2955 2960

AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA 9165
 Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys
 2965 2970 2975

AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT 9213
 Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp
 2980 2985 2990 2995

TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000 3005 3010	9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015 3020 3025	9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 3040	9357
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155	9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170	9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981

Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
 3240 3245 3250
 TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
 Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys
 3255 3260 3265
 AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077
 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val
 3270 3275 3280
 AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125
 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln
 3285 3290 3295
 CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173
 Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys
 3300 3305 3310 3315
 GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330
 TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345
 AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360
 TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375
 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395
 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410
 ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
 340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser

D1
 cont

485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His
 625 630 635 640
 Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
 645 650 655
 Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
 660 665 670
 Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
 675 680 685
 Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
 690 695 700
 Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
 705 710 715 720
 Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
 725 730 735
 Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
 740 745 750
 Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
 755 760 765
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
 770 775 780
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
 785 790 795 800
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
 805 810 815
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
 820 825 830
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
 835 840 845
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
 850 855 860
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
 865 870 875 880
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn
 885 890 895
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
 900 905 910
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
 915 920 925
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
 930 935 940
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
 945 950 955 960
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
 965 970 975

Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys
 980 985 990
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 1040
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 1120
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 1200
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 1280
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 1360
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 1440
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys

1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 1520
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 1600
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 1680
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 1760
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 1840
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 1920
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950

Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 2000
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 2080
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 2160
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 2240
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 2320
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 2400
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys

2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 2480
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 2560
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp
 2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 2640
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
 2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 2720
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 2800
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 2880
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925

D1
 cont

Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 2960
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 3040
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070
 Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 3120
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 3200
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 3280
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 3360
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile

3410

3415

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTTGT GACCGGCGCG GTTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTACC AAGCATGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
Met Pro Ile
1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
20 25 30 35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA 381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
40 45 50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG 429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
55 60 65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG 477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
70 75 80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT 525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
85 90 95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA 573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
100 105 110 115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC 621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
120 125 130

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA 669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln

135										140					145					
TGT	ACA	CAT	GTA	ACA	CCA	CAA	AGA	GAT	AAG	TCA	GTG	GTA	TGT	GGG	AGT	717				
Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val	Cys	Gly	Ser					
150						155						160								
TTG	TTT	CAT	ACA	CCA	AAG	TTT	GTG	AAG	GGT	CGT	CAG	ACA	CCA	AAA	CAT	765				
Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr	Pro	Lys	His					
165						170						175								
ATT	TCT	GAA	AGT	CTA	GGA	GCT	GAG	GTG	GAT	CCT	GAT	ATG	TCT	TGG	TCA	813				
Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met	Ser	Trp	Ser					
180			185						190			195								
AGT	TCT	TTA	GCT	ACA	CCA	CCC	ACC	CTT	AGT	TCT	ACT	GTG	CTC	ATA	GTC	861				
Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val	Leu	Ile	Val					
			200						205			210								
AGA	AAT	GAA	GAA	GCA	TCT	GAA	ACT	GTA	TTT	CCT	CAT	GAT	ACT	ACT	GCT	909				
Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp	Thr	Thr	Ala					
			215			220						225								
AAT	GTG	AAA	AGC	TAT	TTT	TCC	AAT	CAT	GAT	GAA	AGT	CTG	AAG	AAA	AAT	957				
Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu	Lys	Lys	Asn					
230						235						240								
GAT	AGA	TTT	ATC	GCT	TCT	GTG	ACA	GAC	AGT	GAA	AAC	ACA	AAT	CAA	AGA	1005				
Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr	Asn	Gln	Arg					
245						250						255								
GAA	GCT	GCA	AGT	CAT	GGA	TTT	GGA	AAA	ACA	TCA	GGG	AAT	TCA	TTT	AAA	1053				
Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn	Ser	Phe	Lys					
260			265						270			275								
GTA	AAT	AGC	TGC	AAA	GAC	CAC	ATT	GGA	AAG	TCA	ATG	CCA	CAT	GTC	CTA	1101				
Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro	His	Val	Leu					
			280						285			290								
GAA	GAT	GAA	GTA	TAT	GAA	ACA	GTT	GTA	GAT	ACC	TCT	GAA	GAA	GAT	AGT	1149				
Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu	Glu	Asp	Ser					
295						300						305								
TTT	TCA	TTA	TGT	TTT	TCT	AAA	TGT	AGA	ACA	AAA	AAT	CTA	CAA	AAA	GTA	1197				
Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu	Gln	Lys	Val					
310						315						320								
AGA	ACT	AGC	AAG	ACT	AGG	AAA	AAA	ATT	TTC	CAT	GAA	GCA	AAC	GCT	GAT	1245				
Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala	Asn	Ala	Asp					
325						330						335								
GAA	TGT	GAA	AAA	TCT	AAA	AAC	CAA	GTG	AAA	GAA	AAA	TAC	TCA	TTT	GTA	1293				
Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr	Ser	Phe	Val					
340			345						350			355								
TCT	GAA	GTG	GAA	CCA	AAT	GAT	ACT	GAT	CCA	TTA	GAT	TCA	AAT	GTA	GCA	1341				
Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser	Asn	Val	Ala					
			360						365			370								
CAT	CAG	AAG	CCC	TTT	GAG	AGT	GGA	AGT	GAC	AAA	ATC	TCC	AAG	GAA	GTT	1389				
His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser	Lys	Glu	Val					
375						380						385								

GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA 1437
 Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu
 390 395 400

AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT 1485
 Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys
 405 410 415

GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA 1533
 Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg
 420 425 430 435

AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC 1581
 Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser
 440 445 450

CTA CCA AAA TCG GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG 1629
 Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys
 455 460 465

AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA 1677
 Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala
 470 475 480

GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG 1725
 Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln
 485 490 495

GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT 1773
 Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr
 500 505 510 515

TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA 1821
 Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys
 520 525 530

GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA 1869
 Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser
 535 540 545

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG 1917
 Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp
 550 555 560

CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA 1965
 Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu
 565 570 575

ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT 2013
 Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His
 580 585 590 595

GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA 2061
 Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser
 600 605 610

GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA 2109
 Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala
 615 620 625

CCA	CTT	ACA	TTT	GCA	AAT	GCT	GAT	TCA	GGT	TTA	TTG	CAT	TCT	TCT	GTG	2157
Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	Ser	Ser	Val	
		630					635					640				
AAA	AGA	AGC	TGT	TCA	CAG	AAT	GAT	TCT	GAA	GAA	CCA	ACT	TTG	TCC	TTA	2205
Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	Leu	Ser	Leu	
	645					650					655					
ACT	AGC	TCT	TTT	GGG	ACA	ATT	CTG	AGG	AAA	TGT	TCT	AGA	AAT	GAA	ACA	2253
Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	Asn	Glu	Thr	
660					665					670					675	
TGT	TCT	AAT	AAT	ACA	GTA	ATC	TCT	CAG	GAT	CTT	GAT	TAT	AAA	GAA	GCA	2301
Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	Lys	Glu	Ala	
				680					685					690		
AAA	TGT	AAT	AAG	GAA	AAA	CTA	CAG	TTA	TTT	ATT	ACC	CCA	GAA	GCT	GAT	2349
Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	Glu	Ala	Asp	
			695					700					705			
TCT	CTG	TCA	TGC	CTG	CAG	GAA	GGA	CAG	TGT	GAA	AAT	GAT	CCA	AAA	AGC	2397
Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	Pro	Lys	Ser	
		710					715					720				
AAA	AAA	GTT	TCA	GAT	ATA	AAA	GAA	GAG	GTC	TTG	GCT	GCA	GCA	TGT	CAC	2445
Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	Ala	Cys	His	
		725				730					735					
CCA	GTA	CAA	CAC	TCA	AAA	GTG	GAA	TAC	AGT	GAT	ACT	GAC	TTT	CAA	TCC	2493
Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	Phe	Gln	Ser	
740					745					750					755	
CAG	AAA	AGT	CTT	TTA	TAT	GAT	CAT	GAA	AAT	GCC	AGC	ACT	CTT	ATT	TTA	2541
Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	Leu	Ile	Leu	
				760					765						770	
ACT	CCT	ACT	TCC	AAG	GAT	GTT	CTG	TCA	AAC	CTA	GTC	ATG	ATT	TCT	AGA	2589
Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	Ile	Ser	Arg	
			775					780					785			
GGC	AAA	GAA	TCA	TAC	AAA	ATG	TCA	GAC	AAG	CTC	AAA	GGT	AAC	AAT	TAT	2637
Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	Asn	Asn	Tyr	
		790					795					800				
GAA	TCT	GAT	GTT	GAA	TTA	ACC	AAA	AAT	ATT	CCC	ATG	GAA	AAG	AAT	CAA	2685
Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	Lys	Asn	Gln	
	805					810					815					
GAT	GTA	TGT	GCT	TTA	AAT	GAA	AAT	TAT	AAA	AAC	GTT	GAG	CTG	TTG	CCA	2733
Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	Leu	Leu	Pro	
820					825					830					835	
CCT	GAA	AAA	TAC	ATG	AGA	GTA	GCA	TCA	CCT	TCA	AGA	AAG	GTA	CAA	TTC	2781
Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	Val	Gln	Phe	
				840					845					850		
AAC	CAA	AAC	ACA	AAT	CTA	AGA	GTA	ATC	CAA	AAA	AAT	CAA	GAA	GAA	ACT	2829
Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	Glu	Glu	Thr	
			855					860					865			
ACT	TCA	ATT	TCA	AAA	ATA	ACT	GTC	AAT	CCA	GAC	TCT	GAA	GAA	CTT	TTC	2877

Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	Glu	Leu	Phe	
		870					875					880				
TCA	GAC	AAT	GAG	AAT	AAT	TTT	GTC	TTC	CAA	ATA	GCT	AAT	GAA	AGG	AAT	2925
Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Ile	Ala	Asn	Glu	Arg	Asn	
	885					890					895					
AAT	CTT	GCT	TTA	GGA	AAT	ACT	AAG	GAA	CTT	CAT	GAA	ACA	GAC	TTG	ACT	2973
Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	Asp	Leu	Thr	
900					905					910					915	
TGT	GTA	AAC	GAA	CCC	ATT	TTC	AAG	AAC	TCT	ACC	ATG	GTT	TTA	TAT	GGA	3021
Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	Leu	Tyr	Gly	
				920					925					930		
GAC	ACA	GGT	GAT	AAA	CAA	GCA	ACC	CAA	GTG	TCA	ATT	AAA	AAA	GAT	TTG	3069
Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	Lys	Asp	Leu	
			935					940						945		
GTT	TAT	GTT	CTT	GCA	GAG	GAG	AAC	AAA	AAT	AGT	GTA	AAG	CAG	CAT	ATA	3117
Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	Gln	His	Ile	
		950					955					960				
AAA	ATG	ACT	CTA	GGT	CAA	GAT	TTA	AAA	TCG	GAC	ATC	TCC	TTG	AAT	ATA	3165
Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	Leu	Asn	Ile	
	965					970					975					
GAT	AAA	ATA	CCA	GAA	AAA	AAT	AAT	GAT	TAC	ATG	GAC	AAA	TGG	GCA	GGA	3213
Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asp	Lys	Trp	Ala	Gly	
980					985				990					995		
CTC	TTA	GGT	CCA	ATT	TCA	AAT	CAC	AGT	TTT	GGA	GGT	AGC	TTC	AGA	ACA	3261
Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	Phe	Arg	Thr	
			1000						1005					1010		
GCT	TCA	AAT	AAG	GAA	ATC	AAG	CTC	TCT	GAA	CAT	AAC	ATT	AAG	AAG	AGC	3309
Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	Lys	Lys	Ser	
		1015					1020					1025				
AAA	ATG	TTC	TTC	AAA	GAT	ATT	GAA	GAA	CAA	TAT	CCT	ACT	AGT	TTA	GCT	3357
Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	Ser	Leu	Ala	
	1030					1035					1040					
TGT	GTT	GAA	ATT	GTA	AAT	ACC	TTG	GCA	TTA	GAT	AAT	CAA	AAG	AAA	CTG	3405
Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	Lys	Lys	Leu	
	1045				1050					1055						
AGC	AAG	CCT	CAG	TCA	ATT	AAT	ACT	GTA	TCT	GCA	CAT	TTA	CAG	AGT	AGT	3453
Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	Gln	Ser	Ser	
1060				1065					1070					1075		
GTA	GTT	GTT	TCT	GAT	TGT	AAA	AAT	AGT	CAT	ATA	ACC	CCT	CAG	ATG	TTA	3501
Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	Gln	Met	Leu	
			1080						1085					1090		
TTT	TCC	AAG	CAG	GAT	TTT	AAT	TCA	AAC	CAT	AAT	TTA	ACA	CCT	AGC	CAA	3549
Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr	Pro	Ser	Gln	
		1095					1100					1105				
AAG	GCA	GAA	ATT	ACA	GAA	CTT	TCT	ACT	ATA	TTA	GAA	GAA	TCA	GGA	AGT	3597
Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu	Ser	Gly	Ser	

1110 1115 1120

CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG 3645
 Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys
 1125 1130 1135

AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT 3693
 Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr
 1140 1145 1150 1155

TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA 3741
 Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro
 1160 1165 1170

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA 3789
 Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu
 1175 1180 1185

ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT 3837
 Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser
 1190 1195 1200

GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT 3885
 Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe
 1205 1210 1215

TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA 3933
 Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln
 1220 1225 1230 1235

AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT 3981
 Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr
 1240 1245 1250

TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT 4029
 Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp
 1255 1260 1265

TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA 4077
 Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val
 1270 1275 1280

AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA 4125
 Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu
 1285 1290 1295

ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA 4173
 Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg
 1300 1305 1310 1315

AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT 4221
 Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser
 1320 1325 1330

CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT 4269
 His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val
 1335 1340 1345

TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC 4317
 Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn
 1350 1355 1360

ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG 4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln
1365 1370 1375

ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT 4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala
1380 1385 1390 1395

CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT 4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala
1400 1405 1410

ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT 4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe
1415 1420 1425

TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT 4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe
1430 1435 1440

AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC 4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn
1445 1450 1455

TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG 4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met
1460 1465 1470 1475

GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG 4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu
1480 1485 1490

AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG 4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln
1495 1500 1505

GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT 4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly
1510 1515 1520

TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG 4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu
1525 1530 1535

GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA 4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu
1540 1545 1550 1555

ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG 4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu
1560 1565 1570

GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT 4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala
1575 1580 1585

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC 5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn
1590 1595 1600

CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT 5085
 Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn
 1605 1610 1615

TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG 5133
 Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu
 1620 1625 1630 1635

AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT 5181
 Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro
 1640 1645 1650

GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA 5229
 Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser
 1655 1660 1665

GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG 5277
 Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln
 1670 1675 1680

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT 5325
 Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp
 1685 1690 1695

GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG 5373
 Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu
 1700 1705 1710 1715

TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT 5421
 Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His
 1720 1725 1730

CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC 5469
 Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn
 1735 1740 1745

AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC 5517
 Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu
 1750 1755 1760

TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT 5565
 Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val
 1765 1770 1775

GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA 5613
 Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys
 1780 1785 1790 1795

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG 5661
 Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu
 1800 1805 1810

GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT 5709
 Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile
 1815 1820 1825

AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA 5757
 Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala
 1830 1835 1840

TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT 5805

Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile
 1845 1850 1855
 AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG 5853
 Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys
 1860 1865 1870 1875
 GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA 5901
 Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala
 1880 1885 1890
 GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT 5949
 Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser
 1895 1900 1905
 CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC 5997
 Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp
 1910 1915 1920
 ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG 6045
 Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu
 1925 1930 1935
 GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA 6093
 Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser
 1940 1945 1950 1955
 GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT 6141
 Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser
 1960 1965 1970
 GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG 6189
 Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln
 1975 1980 1985
 GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA 6237
 Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile
 1990 1995 2000
 GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC 6285
 Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn
 2005 2010 2015
 GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT 6333
 Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr
 2020 2025 2030 2035
 CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT 6381
 Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn
 2040 2045 2050
 TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC 6429
 Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser
 2055 2060 2065
 ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT 6477
 Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe
 2070 2075 2080
 GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA 6525
 Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg

2085	2090	2095	
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu 2100 2105 2110 2115			6573
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys 2120 2125 2130			6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His 2135 2140 2145			6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160			6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175			6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195			6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210			6861
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225			6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240			6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255			7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275			7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290			7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305			7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320			7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335			7245

GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA 7293
 Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu
 2340 2345 2350 2355

 TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT 7341
 Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser
 2360 2365 2370

 TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT 7389
 Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala
 2375 2380 2385

 ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC 7437
 Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr
 2390 2395 2400

 AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT 7485
 Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val
 2405 2410 2415

 GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA 7533
 Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln
 2420 2425 2430 2435

 AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC 7581
 Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp
 2440 2445 2450

 AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT 7629
 Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala
 2455 2460 2465

 GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT 7677
 Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser
 2470 2475 2480

 CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA 7725
 Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln
 2485 2490 2495

 AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA 7773
 Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr
 2500 2505 2510 2515

 TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT 7821
 Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val
 2520 2525 2530

 CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA 7869
 Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys
 2535 2540 2545

 CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC 7917
 His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His
 2550 2555 2560

 ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA 7965
 Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile
 2565 2570 2575

CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT 8013
 Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala
 2580 2585 2590 2595

GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT 8061
 Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp
 2600 2605 2610

CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC 8109
 Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile
 2615 2620 2625

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT 8157
 Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala
 2630 2635 2640

AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA 8205
 Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg
 2645 2650 2655

TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA 8253
 Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile
 2660 2665 2670 2675

ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT 8301
 Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser
 2680 2685 2690

GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA 8349
 Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys
 2695 2700 2705

ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT 8397
 Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp
 2710 2715 2720

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC 8445
 Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val
 2725 2730 2735

TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA 8493
 Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly
 2740 2745 2750 2755

GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA 8541
 Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro
 2760 2765 2770

GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC 8589
 Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg
 2775 2780 2785

TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG 8637
 Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu
 2790 2795 2800

CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT 8685
 Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp
 2805 2810 2815

GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA 8733

Val	Ile	Ile	Gln	Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu	Lys	Thr	Ser		
2820					2825				2830						2835		
TCT	GGA	TTA	TAC	ATA	TTT	CGC	AAT	GAA	AGA	GAG	GAA	GAA	AAG	GAA	GCA	8781	
Ser	Gly	Leu	Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu	Lys	Glu	Ala		
			2840					2845					2850				
GCA	AAA	TAT	GTG	GAG	GCC	CAA	CAA	AAG	AGA	CTA	GAA	GCC	TTA	TTC	ACT	8829	
Ala	Lys	Tyr	Val	Glu	Ala	Gln	Gln	Lys	Arg	Leu	Glu	Ala	Leu	Phe	Thr		
			2855					2860					2865				
AAA	ATT	CAG	GAG	GAA	TTT	GAA	GAA	CAT	GAA	GAA	AAC	ACA	ACA	AAA	CCA	8877	
Lys	Ile	Gln	Glu	Glu	Phe	Glu	Glu	His	Glu	Glu	Asn	Thr	Thr	Lys	Pro		
		2870						2875				2880					
TAT	TTA	CCA	TCA	CGT	GCA	CTA	ACA	AGA	CAG	CAA	GTT	CGT	GCT	TTG	CAA	8925	
Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg	Ala	Leu	Gln		
		2885						2890				2895					
GAT	GGT	GCA	GAG	CTT	TAT	GAA	GCA	GTG	AAG	AAT	GCA	GCA	GAC	CCA	GCT	8973	
Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala	Asp	Pro	Ala		
2900					2905				2910					2915			
TAC	CTT	GAG	GGT	TAT	TTC	AGT	GAA	GAG	CAG	TTA	AGA	GCC	TTG	AAT	AAT	9021	
Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala	Leu	Asn	Asn		
			2920						2925					2930			
CAC	AGG	CAA	ATG	TTG	AAT	GAT	AAG	AAA	CAA	GCT	CAG	ATC	CAG	TTG	GAA	9069	
His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln	Ile	Gln	Leu	Glu		
			2935						2940					2945			
ATT	AGG	AAG	ACC	ATG	GAA	TCT	GCT	GAA	CAA	AAG	GAA	CAA	GGT	TTA	TCA	9117	
Ile	Arg	Lys	Thr	Met	Glu	Ser	Ala	Glu	Gln	Lys	Glu	Gln	Gly	Leu	Ser		
		2950						2955					2960				
AGG	GAT	GTC	ACA	ACC	GTG	TGG	AAG	TTG	CGT	ATT	GTA	AGC	TAT	TCA	AAA	9165	
Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg	Ile	Val	Ser	Tyr	Ser	Lys		
		2965						2970					2975				
AAA	GAA	AAA	GAT	TCA	GTT	ATA	CTG	AGT	ATT	TGG	CGT	CCA	TCA	TCA	GAT	9213	
Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser	Ile	Trp	Arg	Pro	Ser	Ser	Asp		
2980					2985				2990					2995			
TTA	TAT	TCT	CTG	TTA	ACA	GAA	GGA	AAG	AGA	TAC	AGA	ATT	TAT	CAT	CTT	9261	
Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly	Lys	Arg	Tyr	Arg	Ile	Tyr	His	Leu		
			3000						3005					3010			
GCA	ACT	TCA	AAA	TCT	AAA	AGT	AAA	TCT	GAA	AGA	GCT	AAC	ATA	CAG	TTA	9309	
Ala	Thr	Ser	Lys	Ser	Lys	Ser	Lys	Ser	Glu	Arg	Ala	Asn	Ile	Gln	Leu		
			3015					3020					3025				
GCA	GCG	ACA	AAA	AAA	ACT	CAG	TAT	CAA	CAA	CTA	CCG	GTT	TCA	GAT	GAA	9357	
Ala	Ala	Thr	Lys	Lys	Thr	Gln	Tyr	Gln	Gln	Leu	Pro	Val	Ser	Asp	Glu		
			3030					3035					3040				
ATT	TTA	TTT	CAG	ATT	TAC	CAG	CCA	CGG	GAG	CCC	CTT	CAC	TTC	AGC	AAA	9405	
Ile	Leu	Phe	Gln	Ile	Tyr	Gln	Pro	Arg	Glu	Pro	Leu	His	Phe	Ser	Lys		
		3045						3050				3055					
TTT	TTA	GAT	CCA	GAC	TTT	CAG	CCA	TCT	TGT	TCT	GAG	GTG	GAC	CTA	ATA	9453	
Phe	Leu	Asp	Pro	Asp	Phe	Gln	Pro	Ser	Cys	Ser	Glu	Val	Asp	Leu	Ile		

3060 3065 3070 3075

GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC 9501
 Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val
 3080 3085 3090

TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA 9549
 Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile
 3095 3100 3105

GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC 9597
 Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser
 3110 3115 3120

AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT 9645
 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe
 3125 3130 3135

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT 9693
 Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe
 3140 3145 3150 3155

CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA 9741
 Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile
 3160 3165 3170

CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT 9789
 Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn
 3175 3180 3185

GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC 9837
 Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr
 3190 3195 3200

ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT 9885
 Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser
 3205 3210 3215

CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC 9933
 Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala
 3220 3225 3230 3235

AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG 9981
 Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys
 3240 3245 3250

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG 10029
 Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys
 3255 3260 3265

AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT 10077
 Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val
 3270 3275 3280

AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG 10125
 Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln
 3285 3290 3295

CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA 10173
 Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys
 3300 3305 3310 3315

GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT 10221
 Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile
 3320 3325 3330

TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA 10269
 Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile
 3335 3340 3345

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA 10317
 Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile
 3350 3355 3360

TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT 10365
 Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375

CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395

AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410

ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140

Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met
 180 185 190
 Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val
 195 200 205
 Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp
 210 215 220
 Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu
 225 230 235 240
 Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr
 245 250 255
 Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn
 260 265 270
 Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro
 275 280 285
 His Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu
 290 295 300
 Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu
 305 310 315 320
 Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala
 325 330 335
 Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr
 340 345 350
 Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser
 355 360 365
 Asn Val Ala His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser
 370 375 380
 Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu
 385 390 395 400
 Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile
 405 410 415
 Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu
 420 425 430
 Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg
 435 440 445
 Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val
 450 455 460
 Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys
 465 470 475 480
 Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser
 485 490 495
 Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro
 500 505 510
 Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn
 515 520 525
 Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr
 530 535 540
 Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn
 545 550 555 560
 Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn
 565 570 575
 Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr
 580 585 590
 Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp
 595 600 605
 Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala
 610 615 620
 Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His

625 630 635 640
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr
645 650 655
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg
660 665 670
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr
675 680 685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro
690 695 700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp
705 710 715 720
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala
725 730 735
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp
740 745 750
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr
755 760 765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met
770 775 780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly
785 790 795 800
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu
805 810 815
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu
820 825 830
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys
835 840 845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln
850 855 860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu
865 870 875 880
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn
885 890 895
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr
900 905 910
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val
915 920 925
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys
930 935 940
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys
945 950 955 960
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser
965 970 975
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys
980 985 990
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
995 1000 1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
1010 1015 1020
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
1025 1030 1035 1040
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
1045 1050 1055
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
1060 1065 1070
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
1075 1080 1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
1090 1095 1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
1105 1110 1115 112

D1
cont

Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 1200
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 1280
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 1360
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405
 Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 1440
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 1520
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 1600
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu

D1
 cont

1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 1680
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 1760
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820
 Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 1840
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 1920
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 2000
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 2080
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095

Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 2160
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 2240
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 2320
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 2400
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415
 His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg
 2420 2425 2430
 Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys
 2435 2440 2445
 Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln
 2450 2455 2460
 Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu
 2465 2470 2475 2480
 Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys
 2485 2490 2495
 Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu
 2500 2505 2510
 Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly
 2515 2520 2525
 Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly
 2530 2535 2540
 Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe
 2545 2550 2555 2560
 Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly
 2565 2570 2575
 Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp

2580 2585 2590
 Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro
 2595 2600 2605
 Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr
 2610 2615 2620
 Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys
 2625 2630 2635 2640
 Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu
 2645 2650 2655
 Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 2720
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 2800
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 2880
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 2960
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 3040
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070

Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 3120
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 3200
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 3280
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 3360
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGAGTTTTAC CTCAGTCACA

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAG C

41

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

D1 cont
(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 3FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCTTTAAC TGTTCTGGGT CACA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 3RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAGCATGA CACAATTAAT GA

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other
(B) LOCATION: 1...44
(D) OTHER INFORMATION: 4F/M 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA

44

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

D1 cont (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other
(B) LOCATION: 1...22
(D) OTHER INFORMATION: 4R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCAGATTCA TCTTTATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other
(B) LOCATION: 1...40
(D) OTHER INFORMATION: 5+6F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 5+6R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT

38

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 7F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA

38

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...36
- (D) OTHER INFORMATION: 7R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC

36

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 8F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 8FIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTGCATTCTA GTGATAATAT AC

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 8RIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTGTTAGC AATTTCAAC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGTAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 10AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATAATATA AATTATATGG CTTA

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 10AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT

37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...42
- (D) OTHER INFORMATION: 10BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGTAAAACGA CGGCCAGTAR CTGAAGTGGG ACCAAATGAT AC

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 10BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA

44

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(ii) MOLECULE TYPE: Genomic DNA

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 10CF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 10CRII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGACAGAGGT ACCTGAATC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 11AF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGTAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACCTT

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11AR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT

37

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGAAGCAAA ATGTAATAAG GA

22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22

(D) OTHER INFORMATION: 11BR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CATTAAAGC ACATACATCT TG

22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 11CF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCTAGAGGCA AAGAATCATA C

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11CR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAAGATTATT CCTTTCATTA GC

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11DF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AACCAAAACA CAAATCTAAG AG

22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11DR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCATTTTTA TATGCTGCTT TAC

23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTTTTATAT GGAGACACAG G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
 (A) NAME/KEY: other
 (B) LOCATION: 1...23
 (D) OTHER INFORMATION: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTATTTACAA TTTCAACACA AGC

23

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
 (A) NAME/KEY: other
 (B) LOCATION: 1...20
 (D) OTHER INFORMATION: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATCACAGTTT TGGAGGTAGC

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
 (A) NAME/KEY: other
 (B) LOCATION: 1...21
 (D) OTHER INFORMATION: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGACTTCCT GATTCTTCTA A

21

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCAGATGTT ATTTTCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGTTAAATA ACCAGAAGCA C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGGTAGACAG CAGCAAGC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTAATATCAG TTGGCATTTA TT

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCAGAGGTA CATCCAATAA G

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGTAAA TAGCAAGTCC G

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TACTGAAAAT GAAGATAACA AAT

23

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

D1 cont
(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTTTGTCTT TTCTTATGTC AG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11KF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGTAAACGA CGGCCAGTCT ACTAAACGG AGCAA

35

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11KR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11LF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACAAAATAC TGAAAGAAAG TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCACCACAG TCTCAATAG

19

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11MF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAAGACCC TAAAGTACAG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11MR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATCAAATAT TCCTTCTCTA AG

22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC

35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...35

(D) OTHER INFORMATION: 11NR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT

35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

D1 cont
(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...22

(D) OTHER INFORMATION: 11OF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTACTATAGC TGAAAATGAC AA

22

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...20

(D) OTHER INFORMATION: 11OR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCACTGGCT ATCCTAAATG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGAAGATATT TGC GTTGAGG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTCAGCAAAA ACCTTATGTG

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACGAAAATTA TGGCAGGTTG T

21

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTTGTCCTTGC GTTTTGTAAT G

21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTCATAAG TCAGTCTCAT

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCAAATTCCT CTAACACTCC

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11SF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC

35

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11SR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT

37

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11TF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTCTTCAGA AAATAATCAC TC

22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11TR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGTAAAAAGA GAATGTGTGG C

21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 11UF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTAAAACGA CGGCCAGTAC TTTTCTGAT GTTCCTGTG

39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 11UR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA

39

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...42
- (D) OTHER INFORMATION: 12F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGTAAACGA CGGCCAGTAG TGGTGTTTAA AAGTGGTCAA AA

42

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 12R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA

40

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 13-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAACATTTAA GCATCCGTTA C

21

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...28
- (D) OTHER INFORMATION: 13-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACGAGACT TTTTCATAC TGTATTAG

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACCATGTAGC AAATGAGGGT CT

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCTTTTGTCT GTTTTCCTCC AA

22

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 15-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCAGGGGTTG TGCTTTTAA A

21

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 15FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC

38

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 16AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTGTTTGT TATAATTGTT TTTA

24

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 16AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCAACTTTTT AGTTCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTCAGTATCA TCCTATGTG

19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 17AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGAAACCTTA ACCCATACTG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

D1 cont
(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 18FUT/M13-AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC

39

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 18R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG

38

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...41
- (D) OTHER INFORMATION: 19F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T

41

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

D1 cont
(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 19FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC

39

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 20F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC

38

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39

(D) OTHER INFORMATION: 20R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA

39

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 21F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGTAAAACGA CGGCCAGTGG GTGTTTTATG CTTGGTTCT

39

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 21R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG

40

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 22F-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AACCACACCC TTAAGATGA

19

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 22R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCATTAGTAG TGGATTTTGC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...16
- (D) OTHER INFORMATION: 23FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCACTTCCAT TGCATC

16

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...17
- (D) OTHER INFORMATION: 23RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TGCCAACTGG TAGCTCC

17

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 24 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TACAGTTAGC AGCGACAAAA

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 24R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC

38

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 25F-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCTTTTCGCCA AATTCAGCTA

20

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 25R-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TACCAAAATG TGTGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCACTGAT ACTGGTTTTG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TATACTTACA GGAGCCACAT

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 27AF-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGTGTGTAA TATTTGCG

18

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 27AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG

40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

D1 cont
(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...40

(D) OTHER INFORMATION: 27BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 27BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

38

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1158 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 1...1158

(D) OTHER INFORMATION: Exon 10, nucleotides 31-1146 correspond to nucleotides 1022-2137 of complete coding sequence

(ix) FEATURE

(A) NAME/KEY: variable

(B) LOCATION: 102...602

(D) OTHER INFORMATION: M at positions 102 or 351 = A or C;
R at position 602 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

D1 cont

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TTAATGTGCT TCTGTTTTAT ACTTTAACAG GATTTGGAAA AACATCAGGG AATTCATTTA 60
AAGTAAATAG CTGCAAAGAC CACATTGGAA AGTCAATGCC AMATGTCCTA GAAGATGAAG 120
TATATGAAAC AGTTGTAGAT ACCTCTGAAG AAGATAGTTT TTCATTATGT TTTTCTAAAT 180
GTAGAACAAA AAATCTACAA AAAGTAAGAA CTAGCAAGAC TAGGAAAAAA ATTTTCCATG 240
AAGCAAACGC TGATGAATGT GAAAAATCTA AAAACCAAGT GAAAGAAAAA TACTCATTTG 300
TATCTGAAGT GGAACCAAT GATACTGATC CATTAGATTC AAATGTAGCA MATCAGAAGC 360
CCTTTGAGAG TGGAAGTGAC AAAATCTCCA AGGAAGTTGT ACCGTCCTTG GCCTGTGAAT 420
GGTCTCAACT AACCCTTTCA GGTCTAAATG GAGCCCAGAT GGAGAAAATA CCCCTATTGC 480
ATATTTCTTC ATGTGACCAA AATATTTTCAG AAAAAGACCT ATTAGACACA GAGAACAAAA 540
GAAAGAAAGA TTTTCTTACT TCAGAGAATT CTTTGCCACG TATTTCTAGC CTACCAAAAT 600
CRGAGAAGCC ATTAAATGAG GAAACAGTGG TAAATAAGAG AGATGAAGAG CAGCATCTTG 660
AATCTCATAC AGACTGCATT CTTGCAGTAA AGCAGGCAAT ATCTGGAAT TCTCCAGTGG 720
CTTCTTCATT TCAGGGTATC AAAAAGTCTA TATTCAGAAT AAGAGAATCA CCTAAAGAGA 780
CTTTCATGCA AAGTTTTTCA GGTCAATATGA CTGATCCAAA CTTTAAAAAA GAAACTGAAG 840
CCTCTGAAAG TGGACTGGAA ATACATACTG TTTGCTCACA GAAGGAGGAC TCCTTATGTC 900
CAAATTTAAT TGATAATGGA AGCTGGCCAG CCACCACCAC ACAGAATTCT GTAGCTTTGA 960
AGAATGCAGG TTTAATATCC ACTTTGAAAA AGAAAACAAA TAAGTTTATT TATGCTATAC 1020
ATGATGAAAC ATTTTATAAA GGAAAAAAA TACCGAAAAG CCAAAAATCA GAACTAATTA 1080
ACTGTTTCAGC CCAGTTTGAA GCAAATGCTT TTGAAGCACC ACTTACATTT GCAAATGCTG 1140
ATTCAGGTAC CTCTGTCT 1158
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4987 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 1...4987

(D) OTHER INFORMATION: Exon 11, nucleotides 20-4951 correspond to nucleotides 2138-7069 of complete coding sequence

(ix) FEATURE

(A) NAME/KEY: variable

(B) LOCATION: 339...1917

(D) OTHER INFORMATION: Y at positions 339 or 1917 = C or T;
R at positions 790, 1081 or 1506 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTTGTGTTTT TATGTTTAGG TTTATTGCAT TCTTCTGTGA AAAGAAGCTG TTCACAGAAT 60
 GATTCTGAAG AACCAACTTT GTCCTTAACT AGCTCTTTTG GGACAATTCT GAGGAAATGT 120
 TCTAGAAATG AAACATGTTT TAATAATACA GTAATCTCTC AGGATCTTGA TTATAAAGAA 180
 GCAAAATGTA ATAAGGAAAA ACTACAGTTA TTTATTACCC CAGAAGCTGA TTCTCTGTCA 240
 TGCCTGCAGG AAGGACAGTG TGAAAATGAT CCAAAAAGCA AAAAAGTTTC AGATATAAAA 300
 GAAGAGTCTT TGGCTGCAGC ATGTCACCCA GTACAACAYT CAAAAGTGGA ATACAGTGAT 360
 ACTGACTTTC AATCCCAGAA AAGTCTTTTA TATGATCATG AAAATGCCAG CACTCTTATT 420
 TTAACTCCTA CTTCCAAGGA TGTTCGTCA AACCTAGTCA TGATTTCTAG AGGCAAAGAA 480
 TCATACAAAA TGTCAGACAA GCTCAAAGGT AACAATTATG AATCTGATGT TGAATTAACC 540
 AAAAATATTC CCATGGAAAA GAATCAAGAT GTATGTGCTT TAAATGAAAA TTATAAAGAA 600
 GTTGAGCTGT TGCCACCTGA AAAATACATG AGAGTAGCAT CACCTTCAAG AAAGGTACAA 660
 TTCAACCAAA ACACAAATCT AAGAGTAATC CAAAAAATC AAGAAGAAAC TACTTCAATT 720
 TCAAAAATAA CTGTCAATCC AGACTCTGAA GAACCTTTCT CAGACAATGA GAATAATTTT 780
 GTCTTCCAAR TAGCTAATGA AAGGAATAAT CTTGCTTTAG GAAATACTAA GGAACCTCAT 840
 GAAACAGACT TGACTTGTGT AAACGAACCC ATTTTCAAGA ACTCTACCAT GGTTTTATAT 900
 GGAGACACAG GTGATAAACA AGCAACCCAA GTGTCAATTA AAAAAGATTT GGTTTATGTT 960
 CTTGCAGAGG AGAACAAAAA TAGTGTAAG CAGCATATAA AAATGACTCT AGGTCAAGAT 1020
 TTAAATCGG ACATCTCCTT GAATATAGAT AAAATACCAG AAAAAAATAA TGATTACATG 1080
 RACAAATGGG CAGGACTCTT AGGTCCAATT TCAAAATCACA GTTTTGGAGG TAGCTTCAGA 1140
 ACAGCTTCAA ATAAGGAAAT CAAGCTCTCT GAACATAACA TTAAGAAGAG CAAAATGTTT 1200
 TTCAAAGATA TTGAAGAACA ATATCTACT AGTTTAGCTT GTGTTGAAAT TGTAAATACC 1260
 TTGGCATTAG ATAATCAAAA GAAACTGAGC AAGCCTCAGT CAATTAATAC TGTATCTGCA 1320
 CATTTACAGA GTAGTGTAGT TGTTTCTGAT TGTAATAATA GTCATATAAC CCCTCAGATG 1380
 TTATTTTCCA AGCAGGATTT TAATTCAAAC CATAATTTAA CACCTAGCCA AAAGGCAGAA 1440
 ATTACAGAAC TTTCTACTAT ATTAGAAGAA TCAGGAAGTC AGTTTGAATT TACTCAGTTT 1500
 AGAAARCCAA GCTACATATT GCAGAAGAGT ACATTTGAAG TGCCTGAAAA CCAGATGACT 1560
 ATCTTAAAGA CCACCTCTGA GGAATGCAGA GATGCTGATC TTCATGTCAT AATGAATGCC 1620
 CCATCGATTG GTCAGGTAGA CAGCAGCAAG CAATTTGAAG GTACAGTTGA AATTAAACGG 1680
 AAGTTTGCTG GCCTGTTGAA AAATGACTGT AACAAAAGTG CTTCTGGTTA TTTAACAGAT 1740
 GAAAAATGAAG TGGGGTTTTAG GGGCTTTTAT TCTGCTCATG GCACAAAAC TGAATGTTTCT 1800
 ACTGAAGCTC TGCAAAAAGC TGTGAAACTG TTTAGTGATA TTGAGAATAT TAGTGAGGAA 1860
 ACTTCTGCAG AGGTACATCC AATAAGTTTA TCTTCAAGTA AATGTCATGA TTCTGTYGTT 1920
 TCAATGTTTA AGATAGAAAA TCATAATGAT AAAACTGTAA GTGAAAAAAA TAATAAATGC 1980
 CAACTGATAT TACAAAATAA TATTGAAATG ACTACTGGCA CTTTTGTTGA AGAAATTACT 2040
 GAAAAATTACA AGAGAAATAC TGAAAATGAA GATAACAAAT ATACTGCTGC CAGTAGAAAT 2100
 TCTCATAACT TAGAATTTGA TGGCAGTGAT TCAAGTAAAA ATGATACTGT TTGTATTACT 2160
 AAAGATGAAA CGGACTTGCT ATTTACTGAT CAGCACAACA TATGCTTAA ATTATCTGGC 2220
 CAGTTTATGA AGGAGGGAAA CACTCAGATT AAAGAAGATT TGTCAGATTT AACTTTTTTTG 2280
 GAAGTTGCGA AAGCTCAAGA AGCATGTCAT GGTAATACTT CAAATAAAGA ACAGTTAACT 2340
 GCTACTAAAA CGGAGCAAAA TATAAAAGAT TTTGAGACTT CTGATACATT TTTTCAGACT 2400
 GCAAGTGGGA AAAATATTTAG TGTCGCCAAA GAGTCATTTA ATAAAATTGT AAATTTCTTT 2460
 GATCAGAAAC CAGAAGAATT GCATAACTTT TCCTTAAATT CTGAATTACA TTCTGACATA 2520
 AGAAAGAACA AAATGGACAT TCTAAGTTAT GAGGAAACAG ACATAGTTAA ACACAAAATA 2580
 CTGAAAGAAA GTGTCCCAGT TGGTACTGGA AATCAACTAG TGACCTTCCA GGGACAACCC 2640
 GAACGTGATG AAAAGATCAA AGAACCTACT CTGTTGGGTT TTCATACAGC TAGCGGGAAA 2700
 AAAGTTAAAA TTGCAAAGGA ATCTTTGGAC AAAGTGAAAA ACCTTTTTGA TGA AAAAGAG 2760
 CAAGGTACTA GTGAAATCAC CAGTTTTAGC CATCAATGGG CAAAGACCCT AAAGTACAGA 2820
 GAGGCCTGTA AAGACCTTGA ATTAGCATGT GAGACCATTG AGATCACAGC TGCCCCAAAAG 2880
 TGTAAGAAAA TGCAGAATTC TCTCAATAAT GATAAAAACC TTGTTTCTAT TGAGACTGTG 2940
 GTGCCACCTA AGCTCTTAAG TGATAATTTA TGTAGACAAA CTGAAAATCT CAAAACATCA 3000
 AAAAGTATCT TTTTGAAAGT TAAAGTACAT GAAAATGTAG AAAAAGAAAC AGCAAAAAGT 3060
 CCTGCAACTT GTTACAGAA TCAGTCCCTT TATTGAGTCA TTGAAAATTC AGCCTTAGCT 3120
 TTTTACACAA GTTGTAGTAG AAAAACTTCT GTGAGTCAGA CTTTATTACT TGAAGCAAAA 3180
 AAATGGCTTA GAGAAGGAAT ATTTGATGGT CAACCGAATA GAATAAATAC TGCAGATTAT 3240
 GTAGGAAATT ATTTGTATGA AAATAATTCA AACAGTACTA TAGCTGAAAA TGACAAAAAT 3300
 CATCTCTCCG AAAACAAGA TACTTATTTA AGTAACAGTA GCATGCTTAA CAGCTATTCC 3360
 TACCATTCTG ATGAGGTATA TAATGATTCA GGATATCTCT CAAAAAATAA ACTTGATTCT 3420
 GGTATTGAGC CAGTATTGAA GAATGTTGAA GATCAAAAAA AACTAGTTTT TTCCAAAGTA 3480
 ATATCCAATG TAAAAGATGC AAATGCATAC CCACAAACTG TAAATGAAGA TATTTGCGTT 3540
 GAGGAACCTG TGACTAGCTC TTCACCCTGC AAAAAATAAA ATGCAGCCAT TAAATTGTCC 3600
 ATATCTAATA GTAATAATTT TGAGGTAGGG CCACCTGCAT TTAGGATAGC CAGTGGTAAA 3660

ATCGTTTGTG TTTCACATGA AACAAATTAA AAAGTGAAAG ACATATTTAC AGACAGTTTC 3720
 AGTAAAGTAA TTAAGGAAAA CAACGAGAAT AAATCAAAAA TTTGCCAAAC GAAAATTATG 3780
 GCAGGTTGTT ACGAGGCATT GGATGATTCA GAGGATATTC TTCATAACTC TCTAGATAAT 3840
 GATGAATGTA GCACGCATTC ACATAAGGTT TTTGCTGACA TTCAGAGTGA AGAAATTTTA 3900
 CAACATAACC AAAATATGTC TGGATTGGAG AAAGTTTCTA AAATATCACC TTGTGATGTT 3960
 AGTTTGGAAA CTTTCAGATAT ATGTAAATGT AGTATAGGGA AGCTTCATAA GTCAGTCTCA 4020
 TCTGCAAATA CTTGTGGGAT TTTTAGCACA GCAAGTGGAA AATCTGTCCA GGTATCAGAT 4080
 GCTTCATTAC AAAACGCAAG ACAAGTGTTT TCTGAAATAG AAGATAGTAC CAAGCAAGTC 4140
 TTTTCCAAAG TATTGTTTAA AAGTAACGAA CATTCAGACC AGCTCACAAG AGAAGAAAAAT 4200
 ACTGCTATAC GTACTCCAGA ACATTTAATA TCCCAAAAAG GCTTTTCATA TAATGTGGTA 4260
 AATTCATCTG CTTTCTCTGG ATTTAGTACA GCAAGTGGAA AGCAAGTTTC CATTTTAGAA 4320
 AGTTCCTTAC ACAAAGTTAA GGGAGTGTTA GAGGAATTTG ATTTAATCAG AACTGAGCAT 4380
 AGTCTTCACT ATTCACCTAC GTCTAGACAA AATGTATCAA AAATACTTCC TCGTGTGAT 4440
 AAGAGAAACC CAGAGCACTG TGTAAACTCA GAAATGGAAA AAACCTGCAG TAAAGAATTT 4500
 AAATTATCAA ATAACTTAAA TGTGAAGGT GGTCTTCAG AAAATAATCA CTCTATTAAA 4560
 GTTCTCTCAT ATCTCTCTCA ATTTCAACAA GACAAACAAC AGTTGGTATT AGGAACCAAA 4620
 GTCTCACTTG TTGAGAACAT TCATGTTTTG GGAAAAGAAC AGGCTTCACC TAAAAACGTA 4680
 AAAATGGAAA TTGGTAAAAC TGAAACTTTT TCTGATGTTT CTGTGAAAAC AAATATAGAA 4740
 GTTTGTTCTA CTTACTCCAA AGATTTCAGAA AACTACTTTG AAACAGAAGC AGTAGAAATT 4800
 GCTAAAGCTT TTATGGAAGA TGATGAACTG ACAGATTCTA AACTGCCAAG TCATGCCACA 4860
 CATTCTCTTT TTACATGTCC CGAAAATGAG GAAATGGTTT TGTCAAATTC AAGAATTGGA 4920
 AAAAGAAGAG GAGAGCCCCT TATCTTAGTG GGTAAAGTGT CATTTTTACC TTTCGTGTTG 4980
 CCAATCA 4987

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...468
- (D) OTHER INFORMATION: Exon 14, nucleotides 12-439 correspond to nucleotides 7236-7663 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 248
- (D) OTHER INFORMATION: R at position 248 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCATTGCA GCACAACTAA GGAACGTCAA GAGATACAGA ATCCAAATTT TACCGCACCT 60
 GGTCAAGAAT TTCTGTCTAA ATCTCATTG TATGAACATC TGACTTTGGA AAAATCTTCA 120
 AGCAATTTAG CAGTTTCAGG ACATCCATTT TATCAAGTTT CTGCTACAAG AAATGAAAAA 180
 ATGAGACACT TGATTACTAC AGGCAGACCA ACCAAAGTCT TTGTTCCACC TTTTAAAACT 240
 AAATCACRTT TTCACAGAGT TGAACAGTGT GTTAGGAATA TTAAGTTGGA GGAAAACAGA 300
 CAAAAGCAAA ACATTGATGG ACATGGCTCT GATGATAGTA AAAATAAGAT TAATGACAAAT 360
 GAGATTCAATC AGTTTAACAA AAACAACCTCC AATCAAGCAG CAGCTGTAAC TTTCACAAAG 420
 TGTGAAGAAG AACCTTTAGG TATTGTATGA CAATTTGTGT GATGAATT 468

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 1...255

(D) OTHER INFORMATION: Exon 22, nucleotides 31-229 correspond to nucleotides 8983-9181 of complete coding sequence

(ix) FEATURE

(A) NAME/KEY: variable

(B) LOCATION: 127

(D) OTHER INFORMATION: R at position 127 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTTTTATTCC AATATCTTAA ATGGTCACAG GGTATTTC A GTGAAGAGCA GTTAAGAGCC 60
TTGAATAATC ACAGGCAAAT GTTGAATGAT AAGAAACAAG CTCAGATCCA GTTGGAAATT 120
AGGAAGRCCA TGAATCTGC TGAACAAAAG GAACAAGGTT TATCAAGGGA TGTACAAC 180
GTGTGGAAGT TCGTATTGT AAGCTATTCA AAAAAAGAAA AAGATTCAGG TAAGTATGTA 240
AATGCTTTGT TTTTA 255

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...135

(D) OTHER INFORMATION: Exon 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TAAGTGCATT TTGGTCTTCT GTTTTGCAGA CTTATTTACC AAGCATTGGA GGAATATCGT 60
AGGTAAAAAT GCCTATTGGA TCCAAAGAGA GGCCAACATT TTTTGAAATT TTTAAGACAC 120
GCTGCAACAA AGCAGGTATT GACAAATTTT ATATAAC 157

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 21...269

(D) OTHER INFORMATION: Exon 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGGATTTTTT TTTTAAATAG ATTTAGGACC AATAAGTCTT AATTGGTTTG AAGAACTTTC 60
TTCAGAAGCT CCACCCTATA ATTCTGAACC TGCAGAAGAA TCTGAACATA AAAACAACAA 120
TTACGAACCA AACCTATTTA AAACCTCACA AAGGAAACCA TCTTATAATC AGCTGGCTTC 180

AACTCCAATA ATATTCAAAG AGCAAGGGCT GACTCTGCCG CTGTACCAAT CTCCTGTAAA 240
AGAATTAGAT AAATTCAAAT TAGACTTAGG TAAGTAATGC AATATGGTAG ACTGGGG 297

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 26...134
 - (D) OTHER INFORMATION: Exon 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TCAGTGAATT ATTGTACTGT TTCAGGAAGG AATGTTCCCA ATAGTAGACA TAAAAGTCTT 60
CGCACAGTGA AAATAAAAT GGATCAAGCA GATGATGTTT CCTGTCCACT TCTAAATTCT 120
TGTCTTAGTG AAAGGTATGA TGAAGCTATT ATATTAAAA 159

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 31...71
 - (D) OTHER INFORMATION: Exon 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTAACAATTT TCCCCTTTTT TTACCCCCAG TGGTATGTGG GAGTTTGTTT CATAACACCA 60
AGTTTGTGAA GTTAAATATT 80

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 51...165
 - (D) OTHER INFORMATION: Exon 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TAATGATCAG GGCATTCTA TAAAAAATAA ACTATTTTCT TTCCTCCCAG GGTCGTCAGA 60
CACCAAAACA TATTCTGAA AGTCTAGGAG CTGAGGTGGA TCCTGATATG TCTTGGTCAA 120
GTTCTTTAGC TACACCACCC ACCCTTAGTT CTACTGTGCT CATAGGTAAT AATA 174

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 14...63
- (D) OTHER INFORMATION: Exon 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
TTTTATCTTA CAGTCAGAAA TGAAGAAGCA TCTGAAACTG TATTCCTCA TGATACTACT 60
GCTGTAAGTA AATATGACAT TGATTAGACT                               90
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 20...131
- (D) OTHER INFORMATION: Exon 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TAAACTATAA TTTTTCGAGA ATGTGAAAAG CTATTTTTCCT AATCATGATG AAAGTCTGAA 60
GAAAAATGAT AGATTTATCG CTTCTGTGAC AGACAGTGAA AACACAAATC AAAGAGAAGC 120
TGCAAGTCAT GGTAAGTCCT CT                                         142
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...124
- (D) OTHER INFORMATION: Exon 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
AAAACATATA TGAAATATTT CTTTTTAGGA GAACCCTCAA TCAAAAGAAA CTTATTAAAT 60
GAATTTGACA GGATAATAGA AAATCAAGAA AAATCCTTAA AGGCTTCAAA AAGCACTCCA 120
GATGGTAAAA TTAGCTTTTT ATTTATA                                     147
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...100
- (D) OTHER INFORMATION: Exon 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

AATATGTAAT ATAAAATAAT TGTTTCCTAG GCACAATAAA AGATCGAAGA TTGTTTATGC 60
ATCATGTTTC TTTAGAGCCG ATTACCTGTG TACCCTTTTCG GTAAGACATG TTAAATTTT 120
TCTAA 125

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 13...183
- (D) OTHER INFORMATION: Exon 17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TTATTTGTTT AGGGCTCTGT GTGACACTCC AGGTGTGGAT CCAAAGCTTA TTTCTAGAAT 60
TTGGGTTTAT AATCACTATA GATGGATCAT ATGGAAACTG GCAGCTATGG AATGTGCCTT 120
TCCTAAGGAA TTTGCTAATA GATGCCTAAG CCCAGAAAGG GTGCTTCTTC AACTAAAATA 180
CAGGCAAGTT TAAAGCATT 199

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 19...373
- (D) OTHER INFORMATION: Exon 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

TTTTGTTTTT ACTTTTAGAT ATGATACGGA AATTGATAGA AGCAGAAGAT CGGCTATAAA 60
AAAGATAATG GAAAGGGATG ACACAGCTGC AAAAACAATT GTTCTCTGTG TTTCTGACAT 120
AATTTTCATT AGCGCAAATA TATCTGAAAC TTCTAGCAAT AAAACTAGTA GTGCAGATAC 180
CCAAAAAGTG GCCATTATTG AACTTACAGA TGGGTGGTAT GCTGTTAAGG CCCAGTTAGA 240

TCCTCCCCTC TTAGCTGTCT TAAAGAATGG CAGACTGACA GTTGGTCAGA AGATTATTCT 300
 TCATGGAGCA GAACTGGTGG GCTCTCCTGA TGCCTGTACA CCTCTTGAAG CCCCAGAATC 360
 TCTTATGTTA AAGGTAAATT 380

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 30...185
 - (D) OTHER INFORMATION: Exon 19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

TAAATCAATA TATTTATTAA TTTGTCCAGA TTTCTGCTAA CAGTACTCGG CCTGCTCGCT 60
 GGTATACCAA ACTTGGATTCT TTTCTTGACC CTAGACCTTT TCCTCTGCCC TTATCATCGC 120
 TTTTCAGTGA TGGAGGAAAT GTTGGTTGTG TTGATGTAAT TATTCAAAGA GCATACCCTA 180
 TACAGGTATG ATGTATTCTT GAAACTTA 208

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 28...172
 - (D) OTHER INFORMATION: Exon 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TTTGGTGTGT GTAACACATT ATTACAGTGG ATGGAGAAGA CATCATCTGG ATTATACATA 60
 TTTTCGCAATG AAAGAGAGGA AGAAAAGGAA GCAGCAAAAT ATGTGGAGGC CCAACAAAAG 120
 AGACTAGAAG CCTTATTCAC TAAAATTCAG GAGGAATTTG AAGAACATGA AGGTAAAATT 180
 AGTTATATGG TACACATTGT TATTTC 206

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 36...157
 - (D) OTHER INFORMATION: Exon 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

AGTTTAGTGA ATTAATAATC CTTTGTGTTT CTTAGAAAAC ACAACAAAAC CATATTTACC 60
 ATCACGTGCA CTAACAAGAC AGCAAGTTTC TGCTTTGCAA GATGGTGCAG AGCTTTATGA 120
 AGCAGTGAAG AATGCAGCAG ACCCAGCTTA CCTTGAGGTG AGAGAGTAAG AGGACATATA 180
 ATGAG 185

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 12...175
- (D) OTHER INFORMATION: Exon 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TCTCCAAACA GTTATACTGA GTATTTGGCG TCCATCATCA GATTTATATT CTCTGTTAAC 60
 AGAAGGAAAG AGATACAGAA TTTATCATCT TGCAACTTCA AAATCTAAAA GTAAATCTGA 120
 AAGAGCTAAC ATACAGTTAG CAGCGACAAA AAAAATCTAG TATCAACAAC TACCGGTACA 180
 AACCTTTCAT TGTAATTTTT 200

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 25...163
- (D) OTHER INFORMATION: Exon 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTTTGT TTTGTTTTCT GTAGTTTCA GATGAAATT TATTTAGAT TTACCAGCCA 60
 CGGGAGCCCC TTCACTTCAG CAAATTTTGA GATCCAGACT TTCAGCCATC TTGTTCTGAG 120
 GTGGACCTAA TAGGATTGT CGTTTCTGTT GTGAAAAAAA CAGGTAATGC ACAATATAGT 180
 TAATTTTTTT TATTGATTCT TTTAAAAAAC ATTGTCT 217

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...275
- (D) OTHER INFORMATION: Exon 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TAACATTCTT TTCTTTTTTT TCCATTCTAG GACTTGCCCC TTTCGTCTAT TTGTCAGACG 60
AATGTTACAA TTTACTGGCA ATAAAGTTTT GGATAGACCT TAATGAGGAC ATTATTAAGC 120
CTCATATGTT AATTGCTGCA AGCAACCTCC AGTGGCGACC AGAATCCAAA TCAGGCCTTC 180
TTACTTTTATT TGCTGGAGAT TTTTCTGTGT TTTCTGCTAG TCCAAAAGAG GGCCACTTTC 240
AAGAGACATT CAACAAAATG AAAAATACTG TTGAGGTAAG GTTA 284

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...177
- (D) OTHER INFORMATION: Exon 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ATAAAGCAGC TTTTCCACTT ATTTTCTTAG AATATTGACA TACTTTGCAA TGAAGCAGAA 60
AACAAGCTTA TGCATATACT GCATGCAAAT GATCCCAAGT GGTCCACCCC AACTAAAGAC 120
TGTACTTCAG GGCCGTACAC TGCTCAAATC ATTCCTGGTA CAGGAAACAA GCTTCTGGTA 180
AGTTAATGTA AACTCAAGGA ATATTATAAG 210

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 23...691
- (D) OTHER INFORMATION: Exon 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TACGTTTTCA TTTTATTATC AGATGTCTTC TCCTAATTGT GAGATATATT ATCAAAGTCC 60
TTTATCACTT TGTATGGCCA AAAGGAAGTC TGTTTCCACA CCTGTCTCAG CCCAGATGAC 120
TTCAAAGTCT TGTAAGGGG AGAAAGAGAT TGATGACCAA AAGAACTGCA AAAAGAGAAG 180
AGCCTTGAT TTCTTGAGTA GACTGCCTTT ACCTCCACCT GTTAGTCCCA TTTGTACATT 240
TGTTTCTCCG GCTGCACAGA AGGCATTTC GCCACCAAGG AGTTGTGGCA CCAAATACGA 300
AACACCCATA AAGAAAAAAG AACTGAATTC TCCTCAGATG ACTCCATTTA AAAAATTCAA 360
TGAAATTTCT CTTTGGGAAA GTAATTCAAT AGCTGACGAA GAACCTGCAT TGATAAATAC 420
CCAAGCTCTT TTGTCTGGTT CAACAGGAGA AAAACAATTT ATATCTGTCA GTGAATCCAC 480
TAGGACTGCT CCCACCAAGT CAGAAGATTA TCTCAGACTG AAACGACGTT GTACTACATC 540
TCTGATCAAA GAACAGGAGA GTTCCCAGGC CAGTACGGAA GAATGTGAGA AAAATAAGCA 600
GGACACAATT ACAACTAAAA AATATATCTA AGCATTGCA AAGGCGACAA TAAATTATTG 660
ACGCTTAACC TTTCCAGTTT ATAAGACTGG A 691